Supplementary Material for: Towards a new history and geography of human genes informed by ancient DNA

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Simulation parameters. To generate Figure 1, we performed simulations of different demographic parameters using ms (Hudson, 2002). For the serial bottleneck model in Figure 1A, following a demographic model similar to DeGiorgio et al., 2009, we used the following command to generate 20 haplotypes from each of 42 populations:

20 20 20 20 20 20 -en 0.00114146341463 42 0.025 -ej 0.00134146341463 42 41 -en 0.00248292682927 41 0.025 -ej 0.00268292682927 41 40 -en 0.0038243902439 40 0.025 -ej 0.0040243902439 40 39 -en 0.00516585365854 39 0.025 -ej 0.00536585365854 39 38 -en 0.00650731707317 38 0.025 -ej 0.00670731707317 38 37 -en 0.0078487804878 37 0.025 -ej 0.0080487804878 37 36 -en 0.00919024390244 36 0.025 -ej 0.00939024390244 36 35 -en 0.0105317073171 35 0.025 -ej 0.0107317073171 35 34 -en 0.0118731707317 34 0.025 -ej 0.0120731707317 34 33 -en 0.0132146341463 33 0.025 -ej 0.0134146341463 33 32 -en 0.014556097561 32 0.025 -ej 0.014756097561 32 31 -en 0.0158975609756 31 0.025 -ej 0.0160975609756 31 30 -en 0.0172390243902 30 0.025 -ej 0.0174390243902 30 29 -en 0.0185804878049 29 0.025 -ej 0.0187804878049 29 28 -en 0.0199219512195 28 0.025 -ej 0.0201219512195 28 27 -en 0.0212634146341 27 0.025 -ej 0.0214634146341 27 26 -en 0.0226048780488 26 0.025 -ej 0.0228048780488 26 25 -en 0.0239463414634 25 0.025 -ej 0.0241463414634 25 24 -en 0.025287804878 24 0.025 -ej 0.025487804878 24 23 -en 0.0266292682927 23 0.025 -ej 0.0268292682927 23 22 -en 0.0279707317073 22 0.025 -ej 0.0281707317073 22 21 -en 0.029312195122 21 0.025 -ej 0.029512195122 21 20 -en 0.0306536585366 20 0.025 -ej 0.0308536585366 20 19 -en 0.0319951219512 19 0.025 -ej 0.0321951219512 19 18 -en 0.03333365853659 18 0.025 -ej 0.0335365853659 18 17 -en 0.0346780487805 17 0.025 -ej 0.0348780487805 17 16 -en 0.0360195121951 16 0.025 -ej 0.0362195121951 16 15 -en 0.0373609756098 15 0.025 -ej 0.0375609756098 15 14 -en 0.0387024390244 14 0.025 -ej 0.0389024390244 14 13 -en 0.040043902439 13 0.025 -ej 0.040243902439 13 12 -en 0.0413853658537 12 0.025 -ej 0.0415853658537 12 11 -en 0.0427268292683 11 0.025 -ej 0.0429268292683 11 10 -en 0.0440682926829 10 0.025 -ej 0.0442682926829 10 9 -en 0.0454097560976 9 0.025 -ej 0.0456097560976 9 8 -en 0.0467512195122 8 0.025 -ej 0.0469512195122 8 7 -en 0.0480926829268 7 0.025 -ej 0.0482926829268 7 6 -en 0.0494341463415 6 0.025 -ej 0.0496341463415 6 5 -en 0.0507756097561 5 0.025 -ej 0.0509756097561 5 4 -en 0.0521170731707 4 0.025 -ej 0.0523170731707 4 3 -en 0.0534585365854 3 0.025 -ej 0.0536585365854 3 2 -en 0.0548 2 0.025 -ej 0.055 2 1

In the demographic model in Figure 1B, there are three ancestral populations, two of which experienced strong bottlenecks. All observed populations are mixtures (in different proportions) of two of these populations. To simulate this scenario, we used the following command. The output of this command is 20 haplotypes from 45 populations (the three ancestral populations and the 42 observed populations). For plotting purposes, we ignore the three ancestral populations (populations 0, 22, and 44 in the command).

```
23 -em 0.001475 3 1 36363.6363636 -ej 0.0015 3 23 -em 0.001475 4 1
34545.4545455 -ej 0.0015 4 23 -em 0.001475 5 1 32727.2727273 -ej 0.0015
5 23 -em 0.001475 6 1 30909.0909091 -ej 0.0015 6 23 -em 0.001475 7 1
29090.9090909 -ej 0.0015 7 23 -em 0.001475 8 1 27272.72727 -ej 0.0015
8 23 -em 0.001475 9 1 25454.5454545 -ej 0.0015 9 23 -em 0.001475 10 1
23636.36364 -ej 0.0015 10 23 -em 0.001475 11 1 21818.1818182 -ej
0.0015 11 23 -em 0.001475 12 1 20000.0 -ej 0.0015 12 23 -em 0.001475 13
1 18181.8181818 -ej 0.0015 13 23 -em 0.001475 14 1 16363.6363636 -ej
0.0015 14 23 -em 0.001475 15 1 14545.4545455 -ej 0.0015 15 23 -em
0.001475 16 1 12727.2727273 -ej 0.0015 16 23 -em 0.001475 17 1
10909.0909091 -ej 0.0015 17 23 -em 0.001475 18 1 9090.90909091 -ej
0.0015 18 23 -em 0.001475 19 1 7272.727273 -ej 0.0015 19 23 -em
0.001475 20 1 5454.54545455 -ej 0.0015 20 23 -em 0.001475 21 1
3636.36363636 -ej 0.0015 21 23 -em 0.001475 22 1 1818.18181818 -ej
0.0015 22 23 -em 0.001475 24 23 38181.8181818 -ej 0.0015 24 45 -em
0.001475 25 23 36363.6363636 -ej 0.0015 25 45 -em 0.001475 26 23
34545.4545455 -ej 0.0015 26 45 -em 0.001475 27 23 32727.2727273 -ej
0.0015 27 45 -em 0.001475 28 23 30909.0909091 -ej 0.0015 28 45 -em
0.001475 29 23 29090.9090909 -ej 0.0015 29 45 -em 0.001475 30 23
27272.727277 -ej 0.0015 30 45 -em 0.001475 31 23 25454.5454545 -ej
0.0015 31 45 -em 0.001475 32 23 23636.3636364 -ej 0.0015 32 45 -em
0.001475 33 23 21818.1818182 -ej 0.0015 33 45 -em 0.001475 34 23
20000.0 -ej 0.0015 34 45 -em 0.001475 35 23 18181.8181818 -ej 0.0015 35
45 -em 0.001475 36 23 16363.6363636 -ej 0.0015 36 45 -em 0.001475 37 23
14545.4545455 -ej 0.0015 37 45 -em 0.001475 38 23 12727.2727273 -ej
0.0015 38 45 -em 0.001475 39 23 10909.0909091 -ej 0.0015 39 45 -em
0.001475 40 23 9090.90909091 -ej 0.0015 40 45 -em 0.001475 41 23
7272.72727373 -ej 0.0015 41 45 -em 0.001475 42 23 5454.54545455 -ej
0.0015 42 45 -em 0.001475 43 23 3636.36363636 -ej 0.0015 43 45 -em
0.001475 44 23 1818.18181818 -ej 0.0015 44 45 -en 0.02725 45 0.0025 -ej
0.0275 45 23 -en 0.05475 23 0.0025 -ej 0.055 23 1
```

In the demographic model in Figure 1C, there are three ancestral populations, two of which have admixed with an archaic population in different proportions. All observed populations are mixtures (in different proportions) of two of these populations. To simulate this scenario, we used the following command. The output of this command is 20 haplotypes from 46 populations (the archaic population, the three ancestral populations and the 42 observed populations). For plotting purposes, we ignore the archaic population and the three ancestral populations (populations 0, 22, 44 and 45 in the command):

```
0.0015 18 23 -em 0.001475 19 1 7272.727273 -ej 0.0015 19 23 -em
0.001475 20 1 5454.54545455 -ej 0.0015 20 23 -em 0.001475 21 1
3636.36363636 -ej 0.0015 21 23 -em 0.001475 22 1 1818.18181818 -ej
0.0015 22 23 -em 0.001475 24 23 38181.8181818 -ej 0.0015 24 45 -em
0.001475 25 23 36363.6363636 -ej 0.0015 25 45 -em 0.001475 26 23
34545.4545455 -ej 0.0015 26 45 -em 0.001475 27 23 32727.2727273 -ej
0.0015 27 45 -em 0.001475 28 23 30909.0909091 -ej 0.0015 28 45 -em
0.001475 29 23 29090.9090909 -ej 0.0015 29 45 -em 0.001475 30 23
27272.72727 -ej 0.0015 30 45 -em 0.001475 31 23 25454.5454545 -ej
0.0015 31 45 -em 0.001475 32 23 23636.3636364 -ej 0.0015 32 45 -em
0.001475 33 23 21818.1818182 -ej 0.0015 33 45 -em 0.001475 34 23
20000.0 -ej 0.0015 34 45 -em 0.001475 35 23 18181.8181818 -ej 0.0015 35
45 -em 0.001475 36 23 16363.6363636 -ej 0.0015 36 45 -em 0.001475 37 23
14545.4545455 -ej 0.0015 37 45 -em 0.001475 38 23 12727.2727273 -ej
0.0015 38 45 -em 0.001475 39 23 10909.0909091 -ej 0.0015 39 45 -em
0.001475 40 23 9090.90909091 -ej 0.0015 40 45 -em 0.001475 41 23
7272.72727373 -ej 0.0015 41 45 -em 0.001475 42 23 5454.54545455 -ej
0.0015 42 45 -em 0.001475 43 23 3636.36363636 -ej 0.0015 43 45 -em
0.001475 44 23 1818.18181818 -ej 0.0015 44 45 -em 0.02 23 46 4000 -em
0.020025 23 46 0 -em 0.02 1 46 20000 -em 0.020025 1 46 0 -ej 0.0275 45
23 -ei 0.055 23 1 -ei 1 46 1
```

Admixture tests. To generate Figure 2, we combined SNP data generated on Illumina chips from a number of sources (Li et al., 2008; Altshuler et al., 2010; Behar et al., 2010; Henn et al., 2011; Schlebusch et al., 2012). We excluded the Jewish populations from Behar et al. 2010. In total, the data set consisted of 103 populations and 256,540 SNPs (Supplementary Table 1).

We used ADMIXTOOLS (Patterson et al., 2012) to compute all possible f_3 -statistics of the form $f_3(A; B, C)$ on these populations. We considered an f_3 -statistic to be significant evidence for admixture in population A if it was at least three standard errors less than zero (corresponding to a P-value of about 0.001). In Supplementary Table 1, we list all populations, their approximate latitudes and longitudes, and the representatives of the admixing populations (if any). These representatives were chosen as the population pair B and C that give the minimum f_3 -statistic.

Table 1: Populations used in tests for admixture

Panel	Population	Country	Region	Lat	Long	P1	P2
Pagani	AFAR	Ethiopia	EASTAF	12	41	Sardinian	SUDANESE
Pagani	AMHARA	Ethiopia	EASTAF	10	39	Sardinian	SUDANESE
Pagani	ANUAK ARIBLACKSMIT	Ethiopia	EASTAF	8	34	ARIBLACKSMITH	SUDANESE
Pagani	H ARICULTIVATO	Ethiopia	EASTAF	6	37	NA	NA
Pagani	R	Ethiopia	EASTAF	6	39	Sardinian	Juhoansi
Pagani	ESOMALI	Ethiopia	EASTAF	9	42	Sardinian	SUDANESE
Pagani	GUMUZ	Ethiopia	EASTAF	10.78	35.57	NA	NA
Pagani	OROMO	Ethiopia	EASTAF	8	37	Sardinian	SUDANESE
Pagani	SOMALI	Ethiopia	EASTAF	5.15	46.2	Sardinian	SUDANESE
Pagani	SUDANESE	Sudan	EASTAF	12.86	30.21	NA	NA
Pagani	TYGRAY	Ethiopia	EASTAF	9	38	Sardinian	SUDANESE
Pagani	WOLAYTA	Ethiopia	EASTAF	6	37	MbutiPygmy	Sardinian

				-			
Henn	Khomani	SouthAfrica	SAF	26.97	20.79	Juhoansi	Belorussians
KSP	Khwe	Angola	SAF	-17.4	22.95	Mozabite	Juhoansi
KSP	Xun	Angola	SAF	-14.6	17.66	Yoruba	Juhoansi
KSP	GuiGana	Botswana	SAF	-23.6	24.66	Yoruba	Juhoansi
KSP	Juhoansi	Namibia	SAF	19.59	20.49	NA	NA
KSP	Nama	Namibia	SAF	22.55 -	17.07	Basque	Juhoansi
KSP	Karretjie	SouthAfrica	SAF	30.71	25.10	Russian	Juhoansi
Hgdp	BiakaPygmy	CAR	CAF	4	17	NA	NA
Hgdp	MbutiPygmy	Congo	CAF	1	29	NA	NA
Henn	HADZA	Tanzania	EASTAF	-3.38	36.68	NA	NA
Henn	SANDAWE	Tanzania	EASTAF	-6.18	35.74	Sardinian	Juhoansi
НарМар	LWK	Kenya	EASTAF	0.61	34.76	BiakaPygmy	Sardinian
Hgdp	BantuKenya BantuSouthAfric	Kenya	EASTAF	-3	37	BiakaPygmy	Samaritians
Hgdp	a	SouthAfrica	SAF	-21	18.7	YRI	Juhoansi
НарМар	YRI	Nigeria	WAF	8	5	NA	NA
Hgdp	Yoruba	Nigeria	WAF	8	5	NA	NA
Hgdp	Mandenka	Senegal	WAF	12	-12	NA	NA
НарМар	MKK ColouredWelling	Kenya	EASTAF	-1.32	36.82	MbutiPygmy	Sardinian
KSP	ton	SouthAfrica	SAF	-33.6	19.01	Russian	Juhoansi
Hgdp	Mozabite	Algeria-Mzab Israel-	MIDDLEEAST	32	3	YRI	Sardinian
Hgdp	Druze	Carmel Israel-	MIDDLEEAST	32	35	NA	NA
Hgdp	Palestinian	Central	MIDDLEEAST	32	35	Yoruba	Sardinian
Hgdp	Bedouin	Israel-Negev	MIDDLEEAST	31	35	Sardinian	SUDANESE
НарМар	GIH	India	CSASIA	23	72	Paniya	Georgians
Hgdp	Uygur	China	CSASIA	44	81	Italian	Japanese
Hgdp	Xibo	China	CSASIA	43.5	81.5	Lithuanians	Japanese
Hgdp	Balochi	Pakistan	CSASIA	30.5	66.5	Cypriots	Paniya
Hgdp	Brahui	Pakistan	CSASIA	30.5	66.5	Cypriots	Paniya
Hgdp	Burusho	Pakistan	CSASIA	36.5	74	Georgians	Naxi
Hgdp	Hazara	Pakistan	CSASIA	33.5	70	Italian	Japanese
Hgdp	Kalash	Pakistan	CSASIA	36	71.5	NA	NA BantuSouthAf
Hgdp	Makrani	Pakistan	CSASIA	26	64	Legzins	rica
Hgdp	Pathan	Pakistan	CSASIA	33.5	70.5	Samaritians	Karitiana
Hgdp	Sindhi	Pakistan	CSASIA	25.5	69	Paniya	Georgians
НарМар	CEU	CEPH	NEUROPE	55	-3	Karitiana	Sardinian
НарМар	TSI	Italy	SEUROPE	43	11	Karitiana	Sardinian
Hgdp	French	France	NEUROPE	46	2	Karitiana	Sardinian
Hgdp	Basque	France	SEUROPE	43	0	NA	NA
Hgdp	Italian	Italy	SEUROPE	46	10	Karitiana	Sardinian
Hgdp	Sardinian	Italy	SEUROPE	40	9	NA	NA
Hgdp	Orcadian	Orkney	NEUROPE	59	-3	Karitiana	Sardinian
Hgdp	Russian	Russia Russia-	NEUROPE	61	40	Karitiana	Sardinian
Hgdp	Adygei	Caucasus	NEUROPE	44	39	Karitiana	Sardinian
НарМар	СНВ	China	EASTASIA	32.5	114	Dai	Daur

НарМар	JPT	Japan	NEASTASIA	38	138	NA	NA
Hgdp	Cambodian	Cambodia	EASTASIA	12	105	Dai	Samaritians
Hgdp	Dai	China	EASTASIA	21	100	NA	NA
Hgdp	Daur	China	NEASTASIA	48.5	124	Han	Yakut
Hgdp	Han	China	EASTASIA	32.5	114	Dai	Daur
Hgdp	Hezhen	China	NEASTASIA	47.5	133.5	She	Yakut
Hgdp	Lahu	China	EASTASIA	22	100	NA	NA
Hgdp	Miaozu	China	EASTASIA	28	109	NA	NA
Hgdp	Mongola	China	NEASTASIA	48.5	119	Lithuanians	Japanese
Hgdp	Naxi	China	EASTASIA	26	100	NA	NA
Hgdp	Oroqen	China	NEASTASIA	50.5	126.5	Han	Yakut
Hgdp	She	China	EASTASIA	27	119	NA	NA
Hgdp	Tu	China	EASTASIA	36	101	CEU	Tujia
Hgdp	Tujia	China	EASTASIA	29	109	Dai	Hezhen
Hgdp	Yizu	China	EASTASIA	28	103	NA	NA
Hgdp	Japanese	Japan	EASTASIA	38	138	NA	NA
Hgdp	Yakut	Siberia	NEASTASIA	70	129.5	NA	NA
Hgdp	Melanesian	Bougainville	OCEANIA	-6	155	NA	NA
Hgdp	Papuan	NewGuinea	OCEANIA	-4	143	NA	NA
Hgdp	Karitiana	Brazil	AMERICA	-10	-63	NA	NA
Hgdp	Surui	Brazil	AMERICA	-11	-62	NA	NA
Hgdp	Colombian	Colombia	AMERICA	3	-68	NA	NA
Hgdp	Maya	Mexico	AMERICA	19	-91	Moroccans	Surui
Hgdp	Pima	Mexico	AMERICA	29	-108	NA	NA
Behar	Armenians	Armenia	CAUCASUS	40.07	45.04	GIH	Sardinian
Behar	Belorussians	Belarus	NEUROPE	53.71	27.95	Karitiana	Sardinian
Behar	Chuvaths	Russia	NEUROPE	55.56	46.93	Oroqen	Lithuanians
Behar	Cypriots	Cyprus	SEUROPE	35.13	33.43	Sardinian	ANUAK
Behar	Egyptans	Egypt	NAFRICA	26.82	30.8	Yoruba	Sardinian
Behar	Georgians	Georgia	CAUCASUS	42.32	43.36	NA	NA
Behar	Hungarians	Hungary	NEUROPE	47.16	19.5	Karitiana	Sardinian
Behar	Iranians	Iran	MIDDLEEAST	32.43	53.69	Samaritians	Colombian
Behar	Jordanians	Jordan	MIDDLEEAST	30.59	36.24	Sardinian	SUDANESE
Behar	Legzins	Russia	CAUCASUS	42.14	47.09	Samaritians	Colombian
Behar	Lithuanians	Lithuania	NEUROPE	55.17	23.88	NA	NA
Behar	Moroccans	Morocco	NAFRICA	31.79	-7.09	Yoruba	Sardinian
Behar	North_Kannadi	India	CSASIA	10.85	76.27	NA	NA
Behar	Paniya	India	CSASIA	11.71	76.1	NA	NA
Behar	Romanians	Romania	NEUROPE	45.94	24.97	Karitiana	Sardinian
Behar	Sakilli	India	CSASIA	11.13	78.66	NA	NA
Behar	Samaritians	Israel	MIDDLEEAST	32.07	34.78	NA	NA
Behar	Saudis	SaudiArabia	MIDDLEEAST	23.89	45.08	GuiGana	Sardinian
Behar	Spaniards	Spain	SEUROPE	40.46	-3.75	Karitiana	Sardinian
Behar	Syrians	Syria	MIDDLEEAST	34.8	39	MbutiPygmy	Sardinian
Behar	Turks	Turkey	MIDDLEEAST	38.96	35.24	Karitiana	Sardinian
Behar	Uzbeks	Uzbekistan	CAUCASUS	41.38	64.59	Oroqen	Sardinian
Behar	Yemenese	Yemen	MIDDLEEAST	15.55	48.52	MbutiPygmy	Sardinian